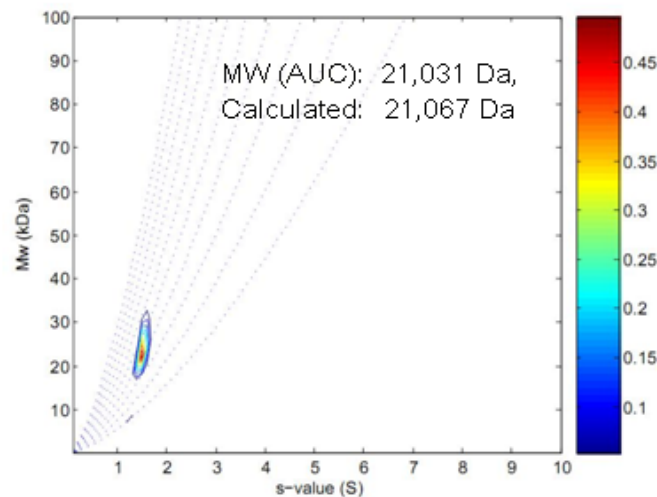
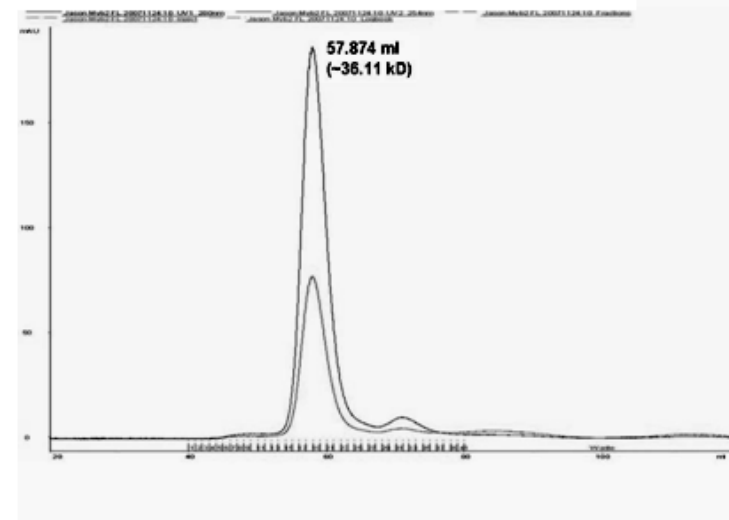


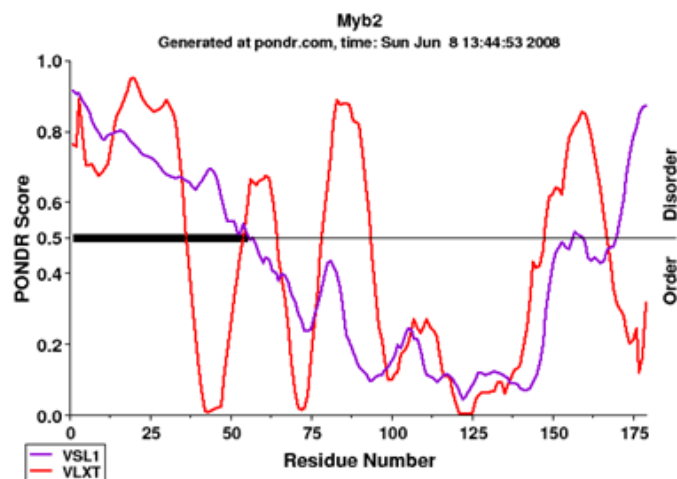
(A) AUC of *t*Myb2



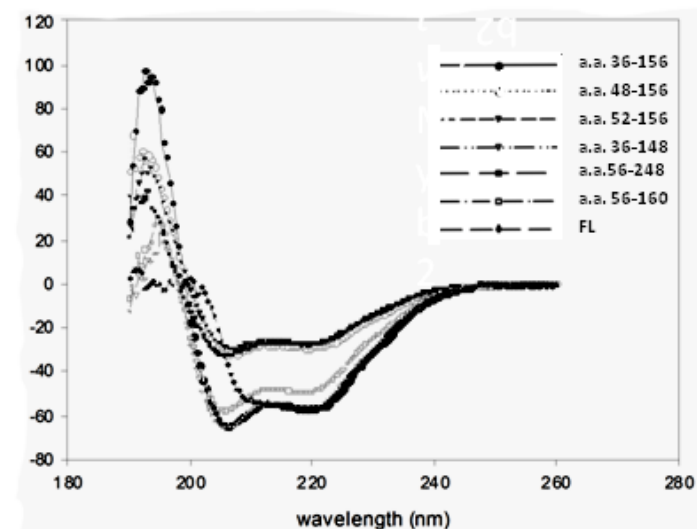
(B) SEC profile of full length *t*Myb2



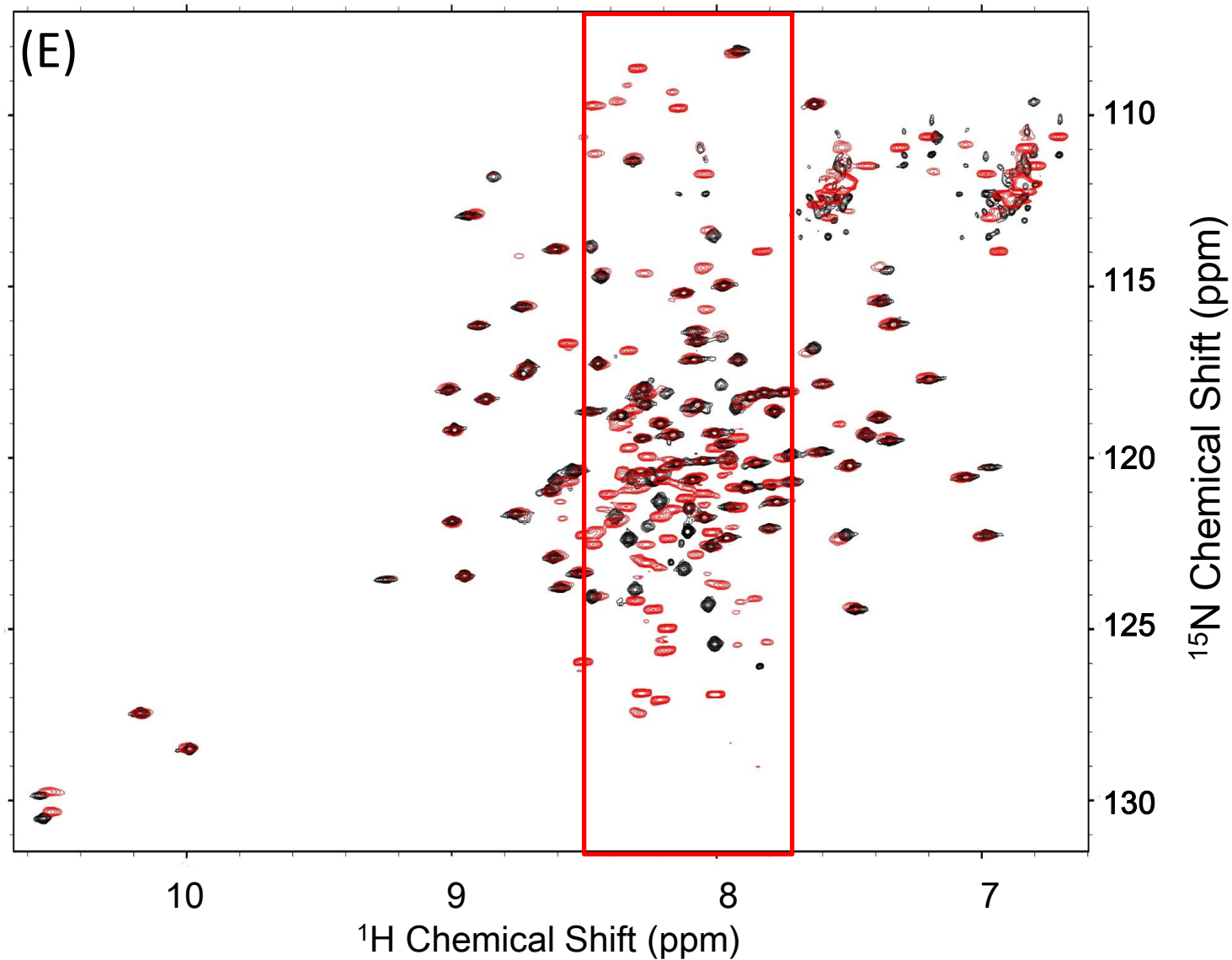
(C) PONDR prediction



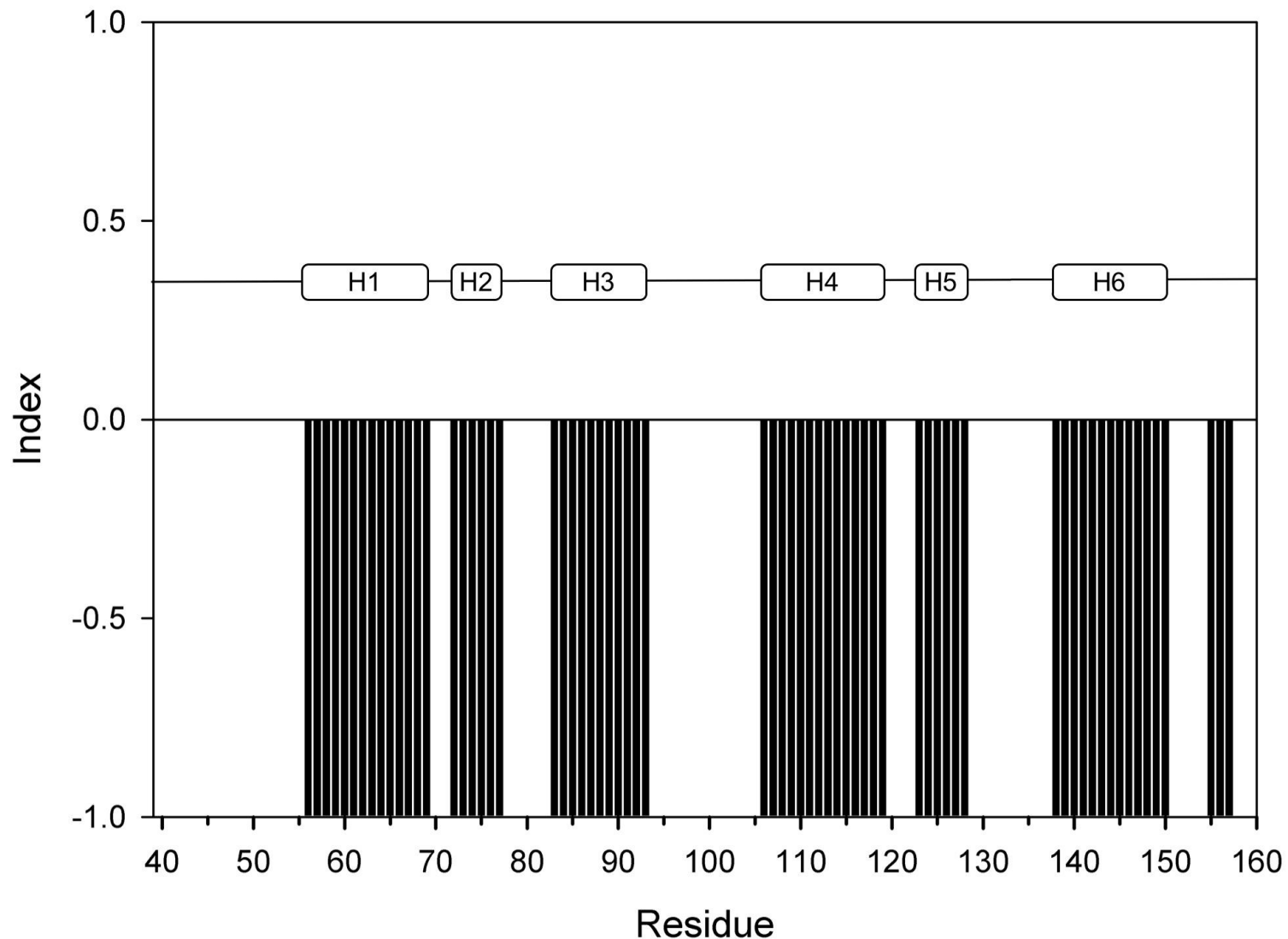
(D) CD of various *t*Myb2 fragments



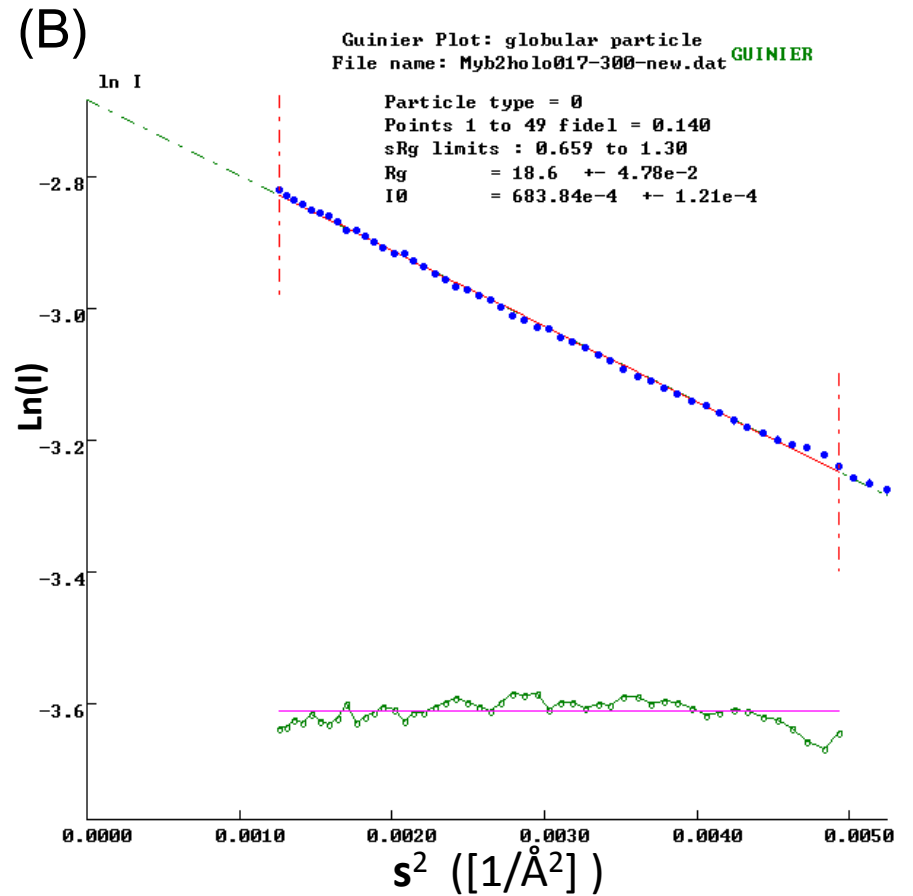
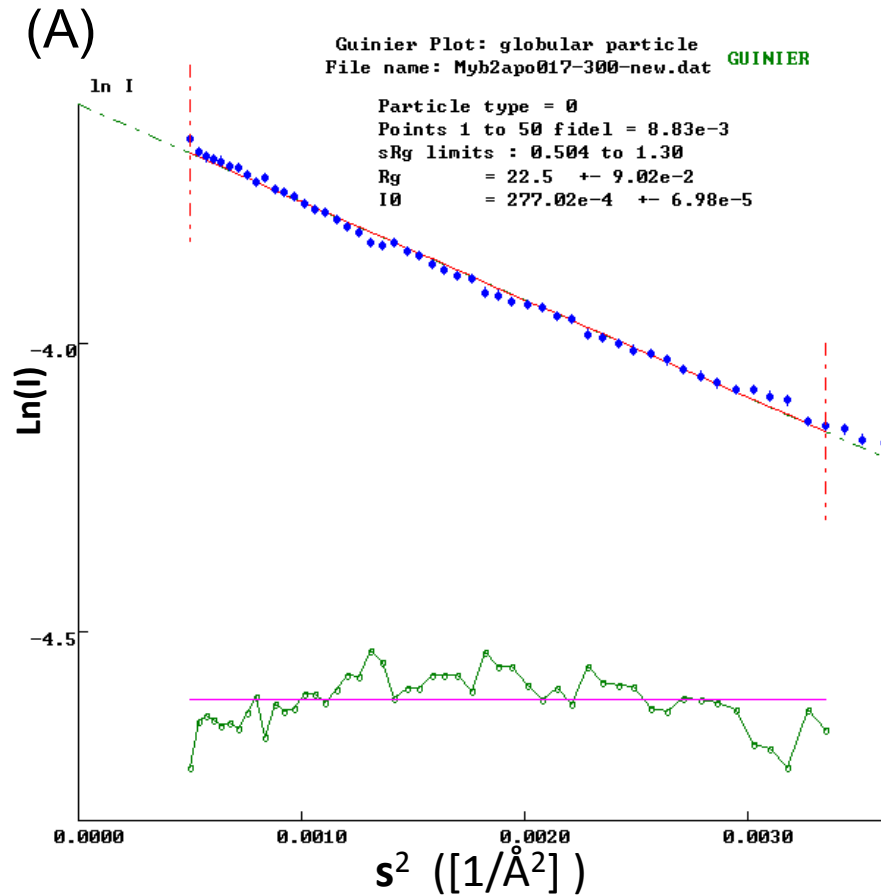
Supplemental Figure S1. (A) Sedimentation equilibrium analytical ultracentrifuge profile of *t*Myb2. The molecular weight estimated is 21,031 Da and that calculated from the sequence is 21,067 Da. (B) Size exclusion chromatograms of *t*Myb2. The estimated molecular weight is 36.1 kDa. (C) PONDR prediction of the order-disorder profile of *t*Myb2. Residues with PONDR score greater than 0.5 are predicted to be disordered and those with less than 0.5 are ordered. (D) CD scans of various *t*Myb2 fragments.



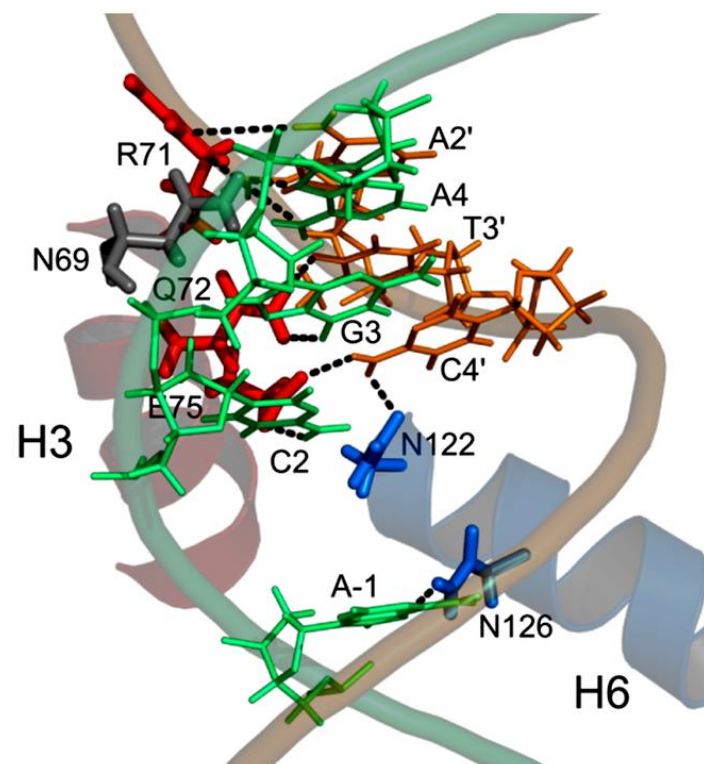
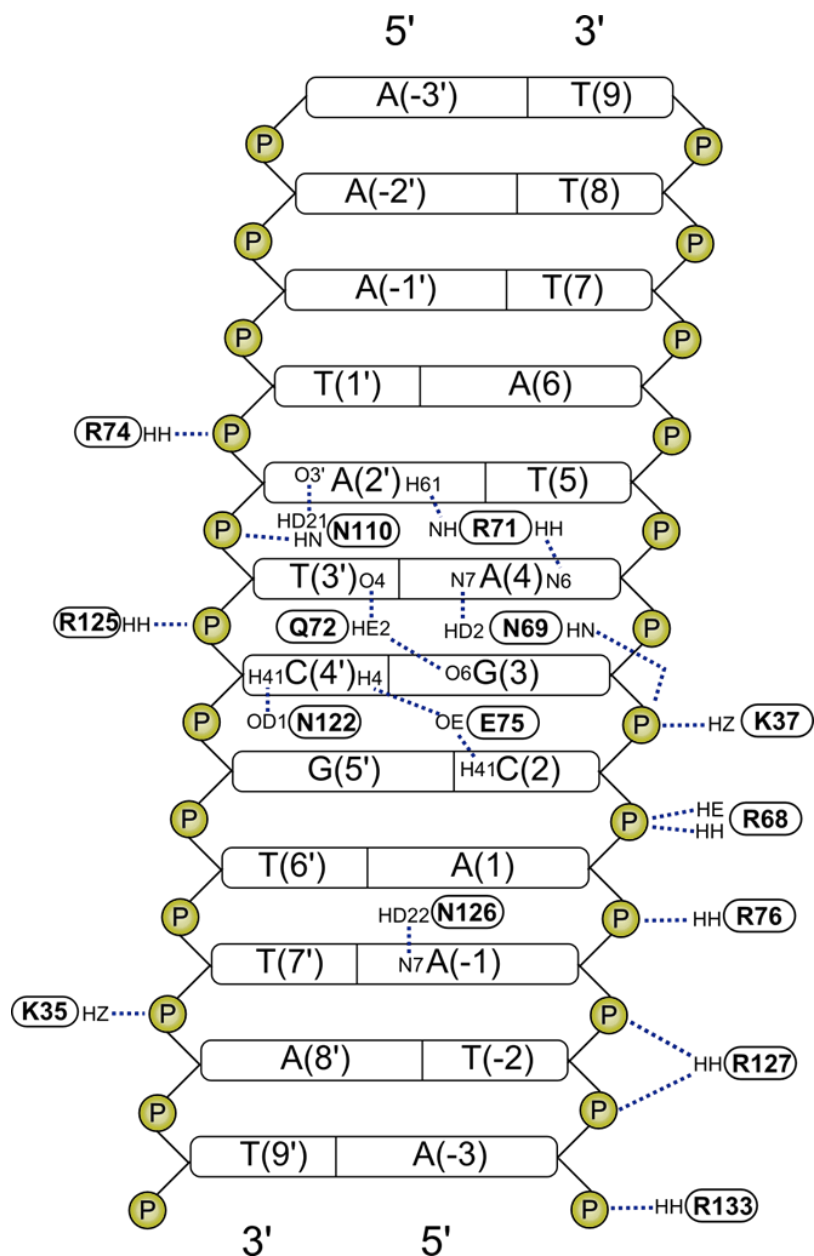
Supplemental Figure S2: ^{15}N -HSQC spectra of the full-length *tMyb2* (red) and *tMyb2*₄₀₋₁₅₆ (black).



Supplemental Figure S3. (Composite chemical shift index derived from H^α , C^α and C^β for assigning the secondary structure of the *t*Myb2₄₀₋₁₅₆-MRE-1-12 complex.



Supplemental Figure S4: Guinier Plots of: (A) DNA-free *t*Myb2₄₀₋₁₅₆; and (B) *t*Myb2₄₀₋₁₅₆. The scattered intensity (*I*) is plotted as a function of scattering angle (s^2), where $s = 4 \cdot \pi \cdot \sin(\theta) / \lambda$, for estimating the *R_g* value.



Supplemental Figure S5: (A) Schematic representations of the detailed interactions between *tMyb1*₃₅₋₁₄₁ with a 16-mer DNA (PDB ID: 2KDZ)